

Attorney's Docket No. 035718/242990 (5718-198)

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re:	Simmons	Confirmation No.:	6779
Appl No.:	10/090,035	Group Art Unit:	1638
Filed:	2/28/02	Examiner:	M. Ibrahim
For:	NUCLEIC ACIDS ENCODING DEFENSE INDUCIBLE PROTEINS AND USES THEREOF		

June 13, 2003

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

SUPPLEMENTAL RESPONSE TO RESTRICTION REQUIREMENT

This Supplemental Response to Restriction Requirement is in response to the Examiner's telephone communications of June 5 and June 12, 2003. For the reader's convenience, the substance of Applicant's Response to Restriction Requirement filed May 22, 2003 has been incorporated herein below.

The Examiner has required restriction between Group I, namely Claims 1-4; Group II, namely Claims 5-8 and 10-12; and Group III, namely Claim 9. Further, for Groups I and II, the Examiner has required restriction between the pairs of polynucleotide sequences set forth in Items A-K. For Group III, Applicant must elect one of the polypeptide sequences of the sequence listing. As indicated in the first Response filed May 22, 2003, Applicant provisionally elected with traverse to prosecute the claims of Group I (Claims 1-4) as drawn to Item A (SEQ ID NO:1 or a nucleotide sequence encoding SEQ ID NO: 2) and expressly reserved the right to file divisional applications or take such other appropriate measures deemed necessary to protect the inventions in the remaining claims.

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Reconsideration of the Requirement for Restriction is Kindly Requested

Applicant maintains the request for reconsideration and modification of the Restriction Requirement because the subject matter should be treated under linking claims practice of 37 C.F.R. § 1.141 and MPEP 809.02. Specifically, Applicant requests that the Restriction Requirement be reconsidered and modified to the extent that the maize sequences of items A-E be considered under linking claim practice, as required by the relevant sections of the MPEP.

The relevant sections of the MPEP state that linking claims are drawn to, and inseparable from, two or more properly divisible inventions. MPEP § 809. The most common types of linking claims which, if allowed, act to prevent restriction between inventions that can otherwise be shown to be divisible, are:

- (A) genus claims linking species claims;
- (B) a claim to the necessary process of making a product linking proper process and product claims;
- (C) a claim to "means" for practicing a process linking proper apparatus and process claims; and
- (D) a claim to the product linking a process of making and a use (process of using).

MPEP § 809.03.

Under linking claim practice, claims linking distinct inventions must be examined with the invention elected, and should any linking claim be allowed, the restriction requirement must be withdrawn. MPEP § 809. Any claim(s) directed to the nonelected invention(s), previously withdrawn from consideration, which depends from or includes all the limitations of the allowable linking claim must be rejoined and will be fully examined for patentability. *Id.*

Applicant's claims qualify for linking claim practice because claim 1 is generic. It contains generic clauses that encompass each of the individual sequences. Thus, although the sequences *are* distinct, they are all linked by claim 1. The Restriction Requirement does not make note of this relationship.

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In the present case, the generic claim is supported by a structural and functional relationship between the sequences that is described as follows in Applicant's disclosure:

A maize disease or stress induced polynucleotide was observed to be highly represented among EST (expressed sequence tags) cDNAs derived from leaf tissue that was either resistant to fungal inoculation or treated with jasmonic acid, a chemical elicitor of plant defense responses. *The maize gene is represented by at least five closely related full-length cDNAs contigs (here termed "alleles") that encode either identical or nearly identical peptides.* A cDNA for one of these "alleles", named ZmAFP1-1 was sequenced. The other four alleles in maize were sequenced in their coding regions. The ORF for the gene predicts a small 10 kDa protein rich in histidine, glycine, and aspartic acid, but with a net neutral pI. Protein domain searching revealed homology to a fly (*Sarcophaga peregrina*) antifungal protein of similar molecular weight (Iijima, R. *et al.*, (1993) *J. Biol. Chem.* 268:12055-12061).

See the specification, paragraph spanning pages 69-70 (emphasis added). These five maize nucleic acid sequences are set forth in SEQ ID NOS:1, 3, 5, 7 and 9 (items A-E of the Restriction Requirement). Further, cDNAs for rice and wheat genes closely homologous to the maize genes were also identified. The rice sequences are set forth in SEQ ID NOS:13 and 15 (items F and G), while the wheat sequences are set forth in SEQ ID NOS:17, 19, 21 and 23 (items H, I, J and K). Based upon this teaching, there is clearly a structural-functional relationship among all of the sequences disclosed in the present application.

Not unexpectedly, the structural relationship is particularly strong between the maize sequences. In support of this, Applicant submits herewith a table that shows the results of an alignment between the maize sequences (Supplemental Exhibit A). In particular, the table shows that SEQ ID NOS:1 and 3 are over 82% identical, SEQ ID NOS:1 and 5 are over 82% identical, SEQ ID NOS:1 and 7 are 75% identical, etc.

To clarify the relationship between the sequences, Applicant has amended the claims. In the first Preliminary Amendment filed May 22, 2003, claim 1 was amended by removing clauses a, b, c, f, and g. In the Supplemental Preliminary Amendment filed contemporaneously herewith, claim 1 has been further amended to recite "[a]n isolated nucleic acid comprising a polynucleotide having at least 75% sequence identity to SEQ ID NO: 1, wherein said polynucleotide encodes a maize AFP1 protein, or a complement of said polynucleotide." Further, Applicant has amended claims 13-17 drawn to the nucleotide sequences of SEQ ID

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NOS:1, 3, 5, 7 and 9, respectively (see the Supplemental Preliminary Amendment, filed concurrently herewith). The amended claims are all within Group I and are drawn to the sequences of Items A-E. Support for the amended claims can be found in the original claims and specification (see the first Preliminary Amendment filed May 22, 2003 and the Supplemental Preliminary Amendment, filed herewith). Applicant emphasizes that the amended claims meet the requirements of MPEP § 809 because claim 1 is generic to each of claims 13-17 and claims 13-17 depend from generic claim 1. Further, claim 1 reads on each of claims 13-17.

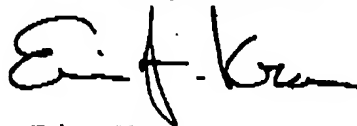
For these reasons, the Restriction Requirement should be reconsidered and modified as follows. First, claims 1-4 and 13-17 as directed to items A-E should be recognized as linked. Under linking claims practice, the generic claim and a first species claim are examined along with the other claims of the group. Accordingly, Applicant requests that claims 1-4 and 13 be examined first. Subsequently, claims 14-17 should be examined as set forth in MPEP § 809, particularly § 809.02.

If the Examiner has further questions or comments with respect to examination of this case, it is respectfully requested that the Examiner telephone the undersigned so that further examination of this application can be expedited.

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It is not believed that extensions of time or fees for net addition of claims are required, beyond those, which may otherwise be provided for in documents accompanying this paper. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 16-0605.

Respectfully submitted,



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CERTIFICATION OF FACSIMILE TRANSMISSION

I hereby certify that this paper is being facsimile transmitted to the US Patent and Trademark Office at Fax No. 703-746-5249 on the date shown below.


Pamela Lockley

June 13, 2003

Date

RTA01/2138102v1

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Alignment of the Malze sequences:

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      1                               50
SEQ ID: 1 (1) --- ACCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 3 (1) --- ACCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 5 (1) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 7 (1) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
SEQ ID: 9 (1) -----AGCG
Consensus (1) ACCACGCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      51                               100
      1 (46) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (48) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (51) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (51) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (5) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (51) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      101                               150
      1 (91) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (98) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (101) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (101) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (55) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (101) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      151                               200
      1 (141) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (148) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (151) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (151) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (105) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (151) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      201                               250
      1 (191) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (198) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (201) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (201) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (155) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (201) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      251                               300
      1 (241) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (248) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (251) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (251) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (205) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (251) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      301                               350
      1 (288) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (295) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (298) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (301) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (252) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (301) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      351                               400
      1 (338) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (345) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (348) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (351) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (302) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (351) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      401                               450
      1 (387) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (394) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (397) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (400) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      9 (352) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
Consensus (401) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT

      451                               500
      1 (437) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      3 (444) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      5 (447) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
      7 (450) TCGACCGTCCGCCACGCGTCCGCACAGCAATCCACACAAGCACT
  
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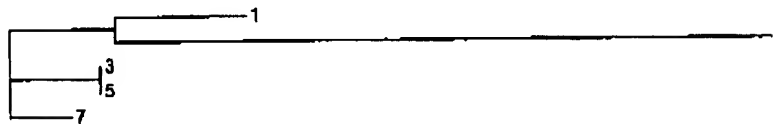
SUPPLEMENTAL EXHIBIT A

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9 (402) -----
Consensus (451) GACTGGTTGT CAGGGTCATCGTACTTGGCTATCGTACGTGCACGCACTC
501 550
1 (487) -----
3 (494) AGCTCGGTACGAATTACGACAATAAGCTGGTGACCTGAAATAAACTTCT
5 (497) AATTCCTGTACGAATTACGACAATAAGCTGGTGACCTGAAATAAACTTCT
7 (500) AGCTCGGTACGAATTACGACAATAAGCTGGTGACCTGAAATAAACTTCT
9 (444) AGCTCGGTACGAATTACGACAATAAGCTGGTGACCTGAAATAAACTTCT
Consensus (501) AGCTCGGTACGAATTACGACAATAAGCTGGTGACCTGAAATAAACTTCT
551 600
1 (537) -----
3 (544) -----
5 (547) -----
7 (550) -----
9 (494) -----
Consensus (551) TCGTAATACTAA AAAAAAAAAAAAAAAAAAAAAA
601 650
1 (587) AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (575) -----
5 (578) -----
7 (581) -----
9 (530) -----
Consensus (601) -----
651 690
1 (637) AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
3 (575) -----
5 (578) -----
7 (581) -----
9 (530) -----
Consensus (651) -----

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Maize Sequences: Gap-like results with Needleman-Wunsch algorithm

SEQ ID NO:	SEQ ID NO:	% Id
1	3	82.1
1	5	82.1
1	7	75
1	9	75

SUPPLEMENTAL EXHIBIT A